TECH CENTER 1600/2900



I hereby certify that the attached papers or fee is being deposited with the United States Postal Service on the date shown below with sufficient postage as first class mail in an envelope addressed to: Assistant Commissioner for Patents, Washington, DC 20231.

Atty. Docket #: 5500*42

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANT: Michel Droux et al.

SERIAL NO: 09/486,334

FILED: July 18, 2000

ART UNIT: 1638

EXAMINER: A. Kubelik

FOR: "Method For Increasing The Content Of Sulphur Compounds And In Particular Of Cysteine, Methoinine

And Glutathione In Plants And Plants Obtained"

Assistant Commissioner for Patents Washington, D.C. 20231

SUBMISSION OF PROPOSED DRAWING AMENDMENTS FOR APPROVAL BY THE EXAMINER

Sir:

Submitted herewith are copies of Figures 1-12 with proposed changes marked in red for the Examiner's approval. In the Office Action of September 10, 2002, the Examiner objected to the drawings because the legends are in French. Changes in the drawings are requested to remove French language legends and words and substitute legends and words in English. Figures 4-7 have also been amended to make the characters more legible in accordance with

Respectfully submitted,

CONNOLLY BOVE LODGE & HUTZ LLP

Date: March 11, 300:

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(302) 888-6420

Attorney for Applicants

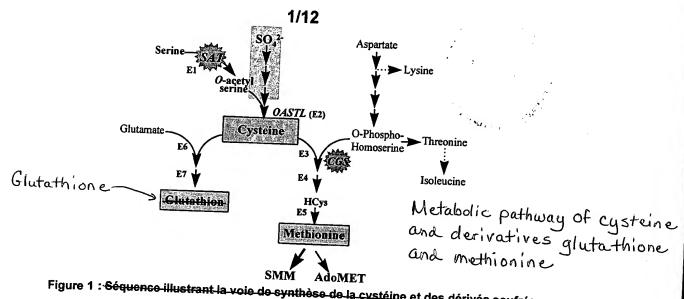
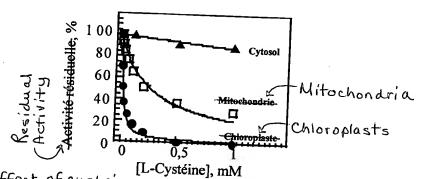


Figure 1 : Séquence illustrant la voie de synthèse de la cystéine et des dérivée soufrés — (glutathion et méthionine).



Effect of cysteine on the activity of serine acety/transferases from pea (Pisum Sativum).

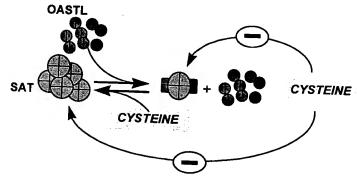


Figure 3: Modèle de l'inhibition de la serine acetyltransferase chloroplastique.

Model of inhibition of chloroplast serine acetyltransferase

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Nucleotide and protein sequences of the SAT3 (L34076) isoform from A. Haliana

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Figure 5: Séquence nucléotidique et peptidique du gène de l'isoforme SAT3' (U30298) d'A.--

Nucleotide and protein sequences of the SAT3' (U30298) isoform from A. Haliana

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R	Y	M	N		F	R	Y	Ρ .	D	R	S .	S	F	N			45
CGT	TAC	ATG	AAC	TAC	TTC	CGT			GAT			TCC		AAT			132
G.	T	Q	T	K	T	L	H	T	R	P	L	L	E	D			60
GGA	ACC	CAG	ACC	AAA	ACC	CTC	CAT	ACT	CGT	CCT	TTG	CTT	GAA				180
L	D	R	D	A	E	V	D	D	V.	W	A	K	I	R			75 225
CTC	GAT	CGC	GAC	GCT	GAA	GTC	GAT	GAT	GTT	TGG	GCC	AAA	ATC	CGA			225
· cr	F.	A	K	S	D	I	A	K	E	P	I	V	S	A			90
GAA	GAG	GCT	AAA	TCT	GAT	ATC	GCC	AAA	GAA	CCT	ATT	GTT	TCC	GCT			270
٧	Y	н	Α	S	I	V	S	Q	R	S	L	E	Α	A			105
TAT	TAT	CAC	GCT	TCG	ATT	GTT	TCT	CAG	CGT	TCG	TTG	GAA	GCT	GCG			315
L	A	N	T	L	S	V	K	L	S	N	L	N	L	P			120
		AAT	ACT	TTA	TCT	GTT	AAA	CTC	AGC	AAT	TTG	AAT	CTT	CCA	*		360
	N	T	L	F	D	L	F	S	G	V	L	Q	G	N			135
AGC	AAC	ACG	CTT	TTC	GAT	TTG	TTC	TCT	GGT	GTT	CTT	CAA	GGA	AAC			405
P	D	I	V	E	S	V	K	L	D	L	L	A	٧	K			150 450 165
CCA	CAT	ATT	GTT	GAA	TÇT	GTC	AAG	CTA	GAT	CTT	TTA	GCT	GTT	AAG			450
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GAG	AGA	GAT	CCT	GCT	TGT	ATA	AGC	TAC	GTT	CAT	TGT	TTC	CTT	CAC			495
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Cuu.	TGG	ACT	CAG	GAC	AGA	AAA	ATC	CTA	GCT	TTG	TTG	ATC	CAG	AAC			585
D	v	S	E	A	F	Α	V	D	F	H	P	G	Α	K			210
AGA	GTC	TCT	GAA	GCC	TTC	GCT	GTT	GAT	TTC	CAC	CCT	GGA	GCT	AAA			630
I	G	T	G	I	L	L	D	H	A	T	Α	I	V	I			225
		ACC	GGG	ATT	TTG	CTA	GAC	CAT	GCT	ACG	GCT	ATT	GTG	ATC			675
a	E	ጥ	A	V ·	V	G	N	N	V	S	I	L	H	N			240
CCT	GAG	ACG	GCG	GTT	GTG	GGG	AAC	AAT	GTT	TCG	ATT	CTC	CAT	AAC			720
V	Т	L	G	G	T	G	K	Q	C	G	D	R	H	P			255
GTT.	ACG	CTT	GGA	GGA	ACG	GGG	AAA	CAG	TGT	GGA	GAT	AGG	CAC	CCG			765
K	I	G	D	G	V	L	I	G	Α	G	T	С	I	L			270
		GGC	GAT	GGG	GTT	TTG	ATT	GGA	GCT	GGG	ACT	TGT	ATT	TTG			810
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GGG	: AAT	ATC	ACG	ATT	GGT	GAA	GGA	GCT	AAG	ATT	GGT	GCG	GGG	TCG			855
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Figure 6: Séquence nucléotidique et peptidique d'un gène de l'isoforme SAT-1' (L78443) d'A.

Nucleotide and protein sequences of the SATI' (L78443) isoform from A. Haliana

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AGC AAC CCT TTC GAT TTC TCT GGT GTT CTT CAA GGA AAC 570 P D I V E S V K L D L L A V K 205 CCA GAT ATT GTC GAG CTA GAG CTA GAT CTT TAA AGC CTA GAT CTT AAG CTT TAA AGC TAC GAT CAT CAA C I AAG CTA GAT CAT GAC GAC GAC GAC CAT GAT CAT GAC CAT GAT CAT CAT GAT CAG CAT GAT CAG CAT GAT CAG CAT CAG CAT GAT CAG CAT GAT CAG CAT CAG CAT GAT CAG CAT CAG CAT CAT TAA									-								
P D I V E S V K L D L L A V K 205 CCA GAT ATT GAT GTC GAG CTA GAT CTT TTA GCT GTT AAG 615 E R D P A C I S Y V H C F L H 220 GAG AGG GAT CTT GAT AGC TAC GTT CTT CAC GA AH R I A H E 235 TTT AAA GGC TCT TGT CAA GCT CAT GGT CAT CAT GGT CAT	_		-	_	_	_	_	_		-	-						
CCA GAT ATT GTT GAA TCT GTC AAG CTA GAT CTT TTA GCT GTT AAG 615 E R D P A C I S Y V H C F L H 220 GAG AGA GAT CCT GCT TGT ATA AGC TAC GTT CAT TGT TCC CAC 660 F K G F L A C Q A H R I A H E 235 TTT AAA GGC TTC CTC GCT TGT CAA GCG CAT CGT ATT GCT CAT GAG 705 L W T Q D R K I L A L L I Q N 250 CTT TGG ACT CAG GAC AGA AAA ATC CTA GCT TTG TTG ATC CAG AAC 750 R V S E A F A V D F H P G A K 265 AGA GTC TCT GAA GCC TTC GCT GTT GAT TTC CAC CGG AGC 775 I G T G I L L D H A T A I V I 280 ATC GGT ACC GGG ATT TTG CTA GAC CAT GCT ACG GCT ACG ACC 795 GGT GAG ACC GGG ATT TTG CTA GAC CAT GCT ACG ACC ACC ACC ACC ACC ACC ACC ACC ACC						-											
E R D P A C I S Y V H C F L H 220 GAG AGG GAT GCT GCT TGT ATA AGC TAC GTT CAT GTT CAC GAG ATA R I A H E 235 TTT AAA GGC TCT CAT TGT CAA GCG CAT CGT ATT GCT 705 TTT AAA GCC CAT GCT TGT CAA AAA ATC CTA GCT GCT GAC AAA ATC CTA GCT TTG ATC CAT CAT GCT TTG ATC CAT GCT GTA ATC CAT GCT ATC CAT GCT ATC CAT CAT GCT ATA ATC CAT GCT ATC GCT ATC ATC ATC	_	_		-													
GAG AGA GAT CCT GCT TGT ATA AGC TAC GTT CAT TGT TTC CAC 660 F K G F L A C Q A H R I A H E 235 TTT AAA GGC TTC CTC GCT TGT CAA GGC CAT CGT ATT GCT CAT GAG 705 L W T Q D R K I L A L I Q N 250 CTT TGG ACC CAG AAA AAA ATC CTA GCT TTG TTG ATC CAG AAC 750 R V S E A F A V D F H P G A K 265 AGA GTC TCT GAA GCC TTC GCT GTT GAT GAT GCT CAG AAC 750 ATC GGT ACC GGG ATT TTG CTA GAT GCT AGA GCT ATT GTT GAT CAG AAC 795 I G T G I L L D H A T A I V I 280 ATC GGT ACC GGG ATT TTG CTA GAC GCT ACG GCT ATT GTG ATC CAG AAC 795 GGT GAG ACC GGG ATT TTG CTA GAC CAT ACG GCT ACG ACC CCT GGA GCT AAA 795 GGT GAG ACC GGG ATT TTG CTA GAC CAT ACG GCT ACG ACC CCG GAG GCT AAA 795 GGT GAG ACC GGG ATT TTG CTA GAC CAT ACG GCT ACG ACC ACG ACC CCG GAG ACC ACC CCG ACC ACG ACC ACG ACC ACG ACC ACG ACC ACC																	
TTT AAA GGC TTC CTC GCT TGT CAA GCG CAT CGT ATT GCT CAT GAG 705 L W T Q D R K I L A L L I Q N 250 CTT TGG ACT CAG GAC AGA AAA ATC CTA GCT TTG TTG ATC CAG AAC 750 R V S E A F A V D F H P G A K 265 AGA GTC TCT GAA GCC TTC GCT GTT GAT TTC CAC CCT GGA GCT AAA 795 I G T G I L L D H A T A I V I 280 ATC GGT ACC GGG ATT TTG CTA GAC CAT GCT ACG GCT ATT GTG ATC 840 GC E T A V V G N N V S I L H N 295 GGT GAG ACG GCG GTT GTG GGG AAC AAT GTT TCC ATT CTC CAT AAC 885 V T L G G G T GGG GAC AAA CAT GTT TCC ATT CTC CAT AAC 885 V T L G G G T G G AAA CAG GGG AAA CAG GAA CAG GAC CAC C	_		_			_	_	_				-		CTT			
L W T Q D R K I L A L L I Q N 250 CTT TGG ACT CAG GAC AGA AAA ATC CTA GCT TTG TTG ATC CAG AAC 750 R V S E A F A V D F H P G A K 265 AGA GTC TCT GAA GCC TTC GCT GTT GAT TTC CAC CCT GGA GCT AAA 795 I G T G I L L D H A T A I V I 280 ATC GGT ACC GGG ATT TTG CTA GAC CAT GCT ACG GCT ATT GTG ATC 840 GE T A V V G N N V S I L H N 295 GGT GAG ACG GCG GTT GTG GGG AAC AAT GTT TCG ATT CTC CAT AAC 885 V T L G G G ATG GGG AAC AAT GTT TCG ATT CTC CAT AAC 885 V T L G G G ACG GTT GTG GGG AAC AAT GTT TCG ATT CTC CAT AAC 885 V T L G G G T G G G AAC AAT GTT TCG ATT CTC CAT AAC 885 AGG ATT GGC GAT GGG GTT TTG ATT GGA GCT GTG ATC CTC CAT AAC 885 AGG ATT GGC GAT GGG GTT TTG ATT GGA GCT GGG ACT TGT TTG ATT TTG 975 G N I T I G E G A K I G A G T C I L 325 AGG ATT GGC GAT GGG GTT TTG ATT GGA GCT GGG ACT TGT ATT TTG 975 G N I T I G E G A K I G A G T C I L 325 AGG ATT GGC GAT GGG GTT TTG ATT GGA GCT AAG ATT GTG GGG TCG 1020 V V L K D V P P R T T A V C N 355 GTG GTG TTG AAA GAC GTG CCG CCG CGT ACG ACG GCT GTT GGA AAT 1065 GTG GTG TTG AAA GAC GTG CCG CCG CGT ACG ACG GCT GTT GGA AAT 1065 CCG GCG AGG TTG CTT GGT GGT AAA GAT AAT CCG AAA ACG CAT GAC 1110 K I P G L T M D Q T S H I S E 385 AAG ATT CCT GGT TTG ACT ATG GAC CAG ACG TCG CAT AAA ACG CAT GAC 1110 K I P G L T M D Q T S H I S E 385 AAG ATT CCT GGT TTG ACT ATG GAC CAG ACG TCG CAT AAA ACG CAT GAC 1110	F	K	G	F	L	A	C '	Q	A	H	R	I	A	Н	E		235
CTT TGG ACT CAG GAC AGA AAA ATC CTA GCT TTG TTG ATC CAG AAC 750 R V S E A F A V D F H P G A K 265 AGA GTC TCT GAA GCC TTC GCT GTT GAT TTC CAC CCT GGA GCT AAA 795 I G T G I L L D H A T A I V I 280 ATC GGT ACC GGG ATT TTG CTA GAC CAT GCT ACG GCT ACG GCT ATC GTG ATC 840 G E T A V V G N N V S I L H N 295 GGT GAG ACG GCG GTT GTG GGG AAC AAT GTT TCG ATT CTC CAT AAC 885 V T L G G T GG GGG AAC AAT GTT TGG ATT CTC CAT AAC 885 K I G D G V L I G A GG ACG GGG AAC AAT GTT TCG ATT TCG ATT TTG 750 AAG ATT GGC GAT GGG GT TTG ATT GAT GGA GCT GGG ACT TGT ATT TTG 930 K I G D G V L I G A G TT GAT GGG GT ACG GCT GGG ACT TGT ATT TTG 975 GAA ATT GGC GAT GGG GT TTG ATT GAT GGA GCT GGG ACT TGT ATT TTG 975 G N I T I G E G A A K I G G G GT ACG GCT GCT GCT GCT GCT GCT 1020 V V L K D V P P P R T T A V G G N 355 GTG GTG TTG AAA GAC GTG CCG CCG CCG CCG CCG GCT GTT GGA AAT 1065 P A R L L G G K D N P K T H D J 370 CCG GCG AGG TTG CTT GGT GGT GAA GAA GAT AAT CCG AAA ACG CAT GAC 1110 K I P G C C GGT TTG ACT ATG GAC CAG ACG TCG CCG AAA ACG CAT GAC 1110 AG ATT CCT GGT TTG ACT ATG GAC CAG A	TTT	AAA	GGC	TTC	CTC	GCT	TGT	CAA	GCG	CAT	CGT	ATT	GCT	CAT	GAG		705 .
R V S E A F A V D F H P G A K 265 AGA GTC TCC GCT GTT GAT TTC CAC CCT GGA GCT AAA 795 I G T G I L L D H A T A I V I 280 ATC GGT ACC GGT GGT ACC CAT GCT ACG GCT ACG GCT ACG GCT ACG ACC ACA ACC CAT ACC CAT CCT CCA ACC CAT	L	W	T	Q	D	R	K	I	L	A	L	L	I	Q	N		250
AGA GTC TCT GAA GCC TTC GCT GTT GAT TTC CAC CCT GGA GCT AAA 795 I G T G I L L D H A T A I V I 280 ATC GGT ACC GGG ATT TTG CTA GAC CAT GCT ACG GCT ATT GTG 840 G E T A V V G N N V S I L H N 295 GGT GAG ACG GGG AAC AAC AAC GTT GTC GAT GAT CAC CAT AAC 885 V T L G G AC ACG AAC GAC GAT AGC CAC CAC CAC CAC CAC CAC CAC<	CTT	TGG	ACT	CAG	GAC	AGA	AAA		CTA	GCT	TTG	TTG	ATC	CAG	AAC		
I G T G I L L D H A T A I V I 280 ATC GGT ACC GGT GCT ACG CCT ACG GCT ATT GTG ATC 840 G E T A V V G N N V S I L H N 295 GGT GAG GCG GGG AAC AAT GTT TCG ATT CTC CAT AAC 885 V T L G G T G AAT GTT CTC CAT AAC 885 V T L G G C G D R H P 310 GT ACG GGA GGG AAA CAG GGA GAC CAG ACG CAC CAC CAC									-	-		_	-		_		265
ATC GGT ACC GGG ATT TTG CTA GAC CAT GCT ACG GCT ATT GTG ACC B40 ACC GCT ACG GCT ATT CTC CAT ACC 885 GGT GGT GTG GGG AAC AAT GTT TCG ATT CTC CAT AAC 885 885 W V T L G GGG AAC AAT GTT TCG ATT CTC CAT AAC 885 W Y C G D R H P 310 ACC GGT ACC CCG GGT ATT ACC CCG GGT ACC CCG GGT ATT AGC CCG GGT AGC CAC CCG GCG GGT ACT TGT ATT TTG ATT TTG ATT TTG ATT GGT ACT ACT ACT ACT																	
G E T A V V G N N V S I L H N 295 GGT GAG ACG GGG AAC AAT GTT TCG ATT CTC CAT AAC 885 V T L G G T G K Q C G D R H P 310 GTT ACG GGA ACG GGG AAA CAG TGT GGA GAC CCG 930 K I G D G V L I G A G T C I L 325 AAG ATT GGG GTT TTG ATT GGG ACT TTG ATT TTG 975 G N I T I G A K I G S 340 </td <td>_</td> <td>-</td> <td>_</td> <td>-</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>-</td> <td></td> <td>-</td> <td></td> <td>-</td> <td></td> <td></td>	_	-	_	-							-		-		-		
GGT GAG GCG GTT GTG GGG AAC AAT GTT TCG ATT CTC CAT AAC 885 V T L G G T G K Q C G D R H P 310 GTT ACG GGA ACG GGG AAA CAG TGT GGA GAC CCG 930 K I G D G V L I G A G T C I L 325 AAG ATT GGG GTT TTG ATT GGG ACT TTG ATT TTG ATT TTG 975 GGG GG TTG TTG 975 GG GG TTG TTG ATT GGA GCT GGG ACT TTG ACT GGG GCT AAG ATT GGG GGG TTG				_									_				
V T L G G T G K Q C G D R H P 310 GTT ACG CTT GGA AAA CAG GGA GAA CAG GGA GAA CAG GGA GAA CAG TGT GGA GAC CCG 930 K I G D W L I G A G T C I L 325 AAG ATT GGC GAT GGG GTT TTG ATT GGA GCT GGG ACT TTG ATT TTG 975 G N I T I G E G A K I G A G S 340 GGG AAT ATT GGT GAA GCT AAG ATT TTT ATT TTT ATT ATT	_	_	_				_	-			_	_					
GTT ACG CTT GGA GGA ACG GGG AAA CAG TGT GGA GAT AGG CAC CCG K I G D G V L I G A G T C I L 325 AAG ATT GGC GAT GGG GTT TTG ATT GGA GCT GGG ACT TGT ATT TTG G N I T I G E G A K I G A G S 340 GGG AAT ATC ACG ATT GGT GAA GGA GCT AAG ATT GGT GCG GGG TCG V V L K D V P P R T T A V G N 355 GTG GTG TTG AAA GAC GTG CCG CCG CGT ACG ACG GCT GTT GGA AAT 1065 P A R L L G G K D N P K T H D 370 CCG GCG AGG TTG CTT GGT GGT AAA GAT AAT CCG AAA ACG CAT GAC 1110 K I P G L T M D Q T S H I S E 385 AAG ATT CCT GGT TTG ACT ATG GAC CAG ACG TCG CAT ATA TCC GAG 1155 W S D Y V I				_													
K I G D G V L I G A G T C I L 325 AAG ATT GGC GAT GGG GTT TTG ATT GGG ATT TTG ATT GGG ATT TTG ATT GGG ATT GGT GAA GGA GCT AAG ATT GGG GGG TCG AAG AATT TTG AAG AATT TTG AAG AATT TCG AAG AATT TTG AATT TTG AATT		_	_								-	_			_		
AAG ATT GGC GAT GGG GTT TTG ATT GGG GCT GGG GCT GGG ACT TTG ATT TTG ATT GGG GCT TTG ATT GTG GGG GCG ACG ATT TTG ATT GTG GCG ACG ACG ACG ACG ACG ACG <td></td>																	
G N I T I G E G A K I G A G S 340 GGG AAT ATC ACG ATT GGA GCT AAG ATT GGG GGG TCG 1020 V V L K D V P P R T T A V G N 355 GTG GTG AAG CCG CCG CGT ACG ACG GCT GTT GGA AAT 1065 P A R L L G G K D N P K T H D 370 CCG GCG AAG AAA GAT AAT CCG AAA ACG CAT GAC 1110 K I P G L T M D Q T																	
GGG AAT ATC ACG ATT GGT GAA GGA GCT AAG ATT GGT GCG GGG TCG 1020 V V L K D V P P R T T T A V G N 355 GTG GTG TTG AAA GAC GTG CCG CCG CGT ACG ACG GCT GTT GGA AAT 1065 P A R L L G G K D N P K T H D 370 CCG GCG AGG TTG CTT GGT GGT AAA GAT AAT CCG AAA ACG CAT GAC 1110 K I P G L T M D Q T S H I S E 385 AAG ATT CCT GGT TTG ACT ATG GAC CAG ACG TCG CAT ATA TCC GAG 1155 W S D Y V I 391																	-
V V L K D V P P R T T A V G N 355 GTG GTG TTG CCG CCG CGT ACG ACG GTT GGA AAT 1065 P A R L L G G K D N P K T H D 370 CCG GCG AGG TAAA GAT AAT CCG AAA ACG CAT GAC 1110 K I P G L T M D Q T S H I S E 385 AAG ATT CCT GAT ATG ACG CAG ACG TCG CAT ATA TCC GAG 1155 W S D Y V I I I I I <td< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></td<>																	
GTG GTG AAA GAC GTG CCG CGT ACG ACG GGT GTT GGA AAT 1065 P A R L L G G K D N P K T H D 370 CCG GCG AGG TTG GGT GGT AAA GAT AAT CCG AAA ACG CAT GAC 1110 K I P G L T M D Q T S H I S E 385 AAG ATT V I <t< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></t<>																	
CCG GCG AGG TTG CTT GGT GGT AAA GAT AAT CCG AAA ACG CAT GAC K I P G L T M D Q T S H I S E 385 AAG ATT CCT GGT TTG ACT ATG GAC CAG ACG TCG CAT ATA TCC GAG W S D Y V I 391	GTG	GTG	TTG	AAA	GAC	GTG	CCG	CCG	CGT	ACG	ACG	GCT	GTT	GGA	AAT		
K I P G L T M D Q T S H I S E 385 AAG ATT CCT GGT TTG ACT ATG GAC CAG ACG TCG CAT ATA TCC GAG 1155 W S D Y V I 391	P	A	R	L	L	G	G	K	D	N	P	K	T	H	D ·		370
AAG ATT CCT GGT TTG ACT ATG GAC CAG ACG TCG CAT ATA TCC GAG W S D Y V I 391	CCG	GCG	AGG	TTG	CTT	GGT	GGT	AAA	GAT	AAT	CCG	AAA	ACG	CAT	GAC		1110
W S D Y V I 391	K	I	P	G	L	T	M	D	Q	T	S	H	I	S	E		385
·	AAG	ATT					ATG	GAC	CAG	ACG	TCG	CAT	ATA	TCC	GAG		
TGG TCG GAT TAT GTA ATT TGA 1176	• • •																391
	TGG	TCG	GAT	TAT	GTA	ATT	TGA									1176	

Figure 7 : Séquence nucleotidique et peptidique d'un gène de l'isoforme SAT 1 (U 22964) d'A. - thaliana.

Nucleotide and protein sequences of the SATI (U 22964) isoform from A. Haliana

				_	_	_	_			_	_	_			,1		e.
M	V_	D	<u> </u>	_ <u>s</u> _	<u> </u>	F	<u> </u>	L	L		A	F	<u> </u>	V CEC	<u>s</u>	⊃.: 16	40
ATG	GTG	GAT													TCT	32	48
L	<u>s</u>	<u>F</u>	V	<u> </u>	S	K	R	V_	C	CAR	S	S mcm	TTA	S TCG	S TCT	32	96
		TTT								GAT P	TCT F	E	S	G	F	48	90
P	W	R	D	M	N	G	D	E	L CTT	CCT	_	GAG		GGT	TTC	40	144
CCT		AGA	_		-			K	S	E	F	D	S	N	L	64	723
E	V	Y	A	K	G	T	H	AAG	_						TTG	. 04	192
GAG	GTT	TAC		S	D	P	I	W	D	A	I	R	E	E	A	80	192
L	D	PCCT	R	_	_	CCT	_	TGG		GCT	_						240
			A	E	K	E	P	I	L	S	S	F	L	Y	A	96	210
K	L	E GAG		_		_	_			AGT		_	TTG	_	GCT	,,,	288
			A	H	D	C	L	E	Q	A	L	G	F	V	L	112	
G	I TO	L TTA										GGG		GTT			336
	N	R	L	0	N	P	T	L	L	A	T	Q	L	L	D	128	
A	N NAC	CGT											CTC	TTG	GAT		384
I	P	Y	G	v	M	M	Н	D	K	G	I.	Q	S	S	I	144	
_	TTT	TAT					CAT	GAC	AAA	GGT	ATT	CAG	AGT	TCG	ATT		432
R	Н	D	L	Q	A	F	K	D	R	D	P	A	С	L	S	160	
CGC	CAT	GAT	CTC	CAG	GCA	TTT	AAA	GAT	CGT	GAT	CCT	GCT	TGT	CTG	TCG		480
Y	S	S	A	I	L	H	L	K	G	Y	H	A	L	Q	A	176	
TAT	AGT	TCT	GCT	ATT	TTA	CAT	CTG	AAG	GGT	TAT	CAT	GCG	TTA	CAA	GCA		528
Y	R	V	A	H	K	L	W	N	E	G	R	K	L	L	Α	192	
TAT	AGG	GTT	GCG	CAT	AAA	CTG	TGG	AAT									576
L	A	L.	Q	S	R	I	S	E	V	F	G	I	D	I.	H	208	
CTT	GCA	TTG	CAA	AGC													624
P	Α	A	R	I	G	E	G	I	L	L	D	H	G	T	G	224	670
CCA	GCG	GCA											GGA	ACT	GGA L	240	672
V	V	I	G	E	T	A	V	I	G	N	G	V	S		_	240	720
		ATT			_			G	K	E	T	G	D	R	H	256	720
H	G	V	T	L	G	G	T	GGA								230	768
		GTG I	G	E	G	A	L	L	G	A	C	V	T	I	L	272	, 00
P	K	ATA	_	-	-	-,-		CTT	-			GTG			_		816
	. AAG N	I	S	I	G	A	G	A	M	V	Α.	A	G	s	L	288	
G		ATA						GCA		-			GGT	TCA	CTT		864
V	L	K	D	V	P	S	Н	S	V	V	Α	G	N	P	A	304	
		AAA	GAC	GTT	CCT	TCG	CAT	AGT	GTG	GTG	GCT	GGA	AAT	CCT	GCA		912
K	L	I	R	V	M	E	E	Q .	D		S	\mathbf{L}	Α	M	K	320	
AAA		ATC	AGG	GTC	ATG	GAA	GAG	CAA	GAC	CCG	TCT	CTA	GCA	ATG	AAA		960
H	D	A	T .	K	E	F	F	R	H	V.	Α	D	G	Y	K	336	
	GAT	GCT	ACT	AAA	GAG	TTC	TTT	CGA	CAT	GTA	GCT				AAA	•	1008
G	A	Q	S	N	Ġ	P	S	L	S	A	G	D	T	E	K	352	
GGG	GCA	CAA	TCT	AAC	GGA	CCA	TCA	CTT	TCA	GCA	GGA	GAT	ACA	GAG	AAA		1056
.G	H	T	N	S.	T	S										359	
GGA	CAC	ACT	AAC	AGC	ACA	TCA	TGA										1104

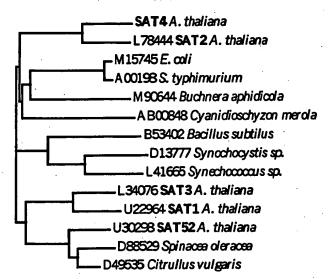
Figure 8: Sequence nucléotidique et peptidique du m RNA de la serine acetyltransferase SAT 2-putative— -chloroplastique d'*Arabidopsis thaliana* (L78444)...

Nucleotide and protein sequences from mRNA of the putative chloroplast serine acetyltransferase SAT2 from Arabidopsis thaliana (L78444)

M	A	C	I	N	G	E	N	R	D	F_	8	8	S	S	15	
	GCT	TGT	ATA			GAG	AAT	CGT	GAT	TTT	TCT	TCC	TCG	TCA	3	45
	L	s	s	L	P	M	I	V	S	R	N	F	S	A	15 30 45	. 15
B mcm	TTC	TCT				ATG	ATT	GTC	TCC	CGG	AAC	TTT	TCT	GCC	33 47	³⁶ '90 -
	D	D	G	E	T	G	D ·	Ε .	F	P	F	E	R.	I	45	
R	GAC	GAT					_		TTT	CCT	TTC	GAG	AGG	ATT		135
F	P	V	Y	A	R	G	T	L	N	P	V	A	D	P	60	
_	CCG	-				GGA				CCC	GTG	GCC	GAC	CCG		180
V	L	L	D	F	T	N	S	S	Y	D	P	I	W.	D	75	
	_	CTG	_			AAT			TAT	GAC	CCA	ATT	TGG	GAT		225
	I	R	E	E	A	K	L	E	A	E	E	E	P	v	90	
S	ушу Т	AGA	GAA	GAA							GAG	GAG	CCG	GTT		270
	S	S	F	L	Y	A	S	I	L	S	H	D ·	C ·	L	105	
L		AGC		_	_	GCT	_	_	_	-	CAT	GAC	TGT	TTA		315
	Q	A	L	s	F	v	L	A	N	R	L	Q	N	P	120	
E	CAA			-	_		CTA				CTC		AAC	CCT		360
	L	L	A	T	Q	L	M	D	I	F	C	N	V	M	135	
T ACĊ	_					CTT		_				AAC	GTT	ATG		405
	H	D	R	G	I	Q	s	S	I	R	L	D	V	Q.	150	
V	CAT					CAA		_			CTT	GAT	GTT	CAG		450
	F	K	D	R	D	P	A	C	L	S	Y	S	S	A	165	
A		AAA			_				CTA	_	_	AGT	TCG	GCT	•	495
	L	H	L	K	G	Y	L	A	L	Q	A	Y	R	V	180	
I	шшу Ti	CAT										TAT	AGA	GTA		540
_	H	K	L	W	K	Q	G	R	K	L	L.	A	L	A	195	
A	CAT						_				TTA	GCA	TTG	GCA	•	585
L	Q	S	R	V	S	E	V	R	T .	A	٧	I	G	D	210	
CALC:	CDA	AGC								GCT	GTG	ATA	GGC	GAC		630
R	V	S	I	L	Н	G	V	T	L	G.	G	T	G	K	225	
	GTC		_			GGT	GTG	ACA	TTA	GGA	GGA	ACT	GGG	AAA		675
E	T	G	D	R	Н	P	N	I	G	D	G [°]	A	\mathbf{L}_{\perp}	L	240	
_	ACC	-	GAC	CGC	CAT	CCA	AAT	ATA	GGC	GAC	GGT	GCT	CTT	CTT		720
G	A	C	V	T	I	L	G	N	I	K	I	G	A	G	255	
GGZ		TGT	GTG	ACT	ATA	CTT	GGT	AAC	ATT	AAG	ATA	GGC	GCT	GGA		765
A	M	V	A	A	G	S	L	V	L	K	D	V	P	S	270	
		GTA	GCT	GCT	GGT	TCG	CTT	GTG	TTA	AAG	GAT	GTT	CCT	TCG		810
H	s	M	V	A	G	N	P	A	K	L	I	G	F	V	285	
CAT	_	ATG	GTG	GCT	GGA	AAT	CCA	GCA	AAA	CTC	ATC	GGG	TTT	GTT		855
D	F.	0	D	P	S	M	T	M	E	H	G	E	S	٠.	299	
GA?	GAG	CAA	GAT	CCA	TCT	ATG	ACA	ATG	GAG	CAT	GGT	GAG	TCT	TGA		900

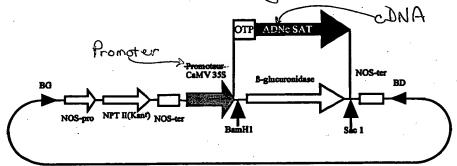
Figure 9: Sequence nucleotidique et en acides aminés du mRNA de la SAT4 putative chloroplastique d'Arabidepsis theliana.

Nucleotide and amino acid sequences from mRNA Of the putative chloroplast SAT4 from Arabidopsis thaliana



Sequence Comparison of serine acetyltransferases from Figure 10 Dendogramme des serine acétyltransferase issues de plusieurs organismes.

A. thaliana and other organisms



Process for insertion of OTP/serine acety/transferase SAT3

Figure 11: Procedure de clonage de l'OTP/Serine acety/transferase SAT3 ou SAT
or cysteine - insensitive SAT such as truncated SAT I in the
(insensible à la cystéine, par exemple SAT1 tronqué) dans le vecteur pBI121.

Vector pBI 121

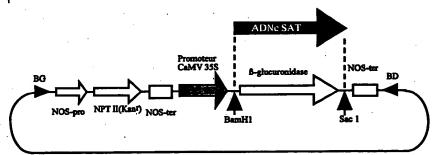


Figure 12: Procédure de clonage de la Serine acétyltransférase SAT1*; SAT1; SAT2; SAT3, SAT3; SAT4, ou toutes SATs dans le vecteur pBI121.

Process for insertion of serine acetyltransferase SATI', SATI, SATI, SATI, SATI, SATI, SATI or any SATI in the vector pBIIII